



8

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) Nico Cerletti

(ii) TITLE OF INVENTION: New process for the production of
biologically active protein

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS

(A) ADDRESSEE: Novartis Patent Department
(B) STREET: 564 Morris Avenue
(C) CITY: Summit
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07901

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/776,444
(B) FILING DATE: 24-JAN-97

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/EP95/02719
(B) FILING DATE: 12-Jul-95
(A) APPLICATION NUMBER: EPO 94810439.3
(B) FILING DATE: 25-Jul-94

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 22640
(C) REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (908) 522-6940
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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPLMu.htGF-beta1 (DSM 5656)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..336

(D) OTHER INFORMATION:/product= "human TGF-beta1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCC CTG GAC ACC AAC TAT TGC TTC AGC TCC ACG GAG AAG AAC TGC TGC	48
Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys	
1 5 10 15	
GTG CGG CAG CTG TAC ATT GAC TTC CGC AAG GAC CTC GGC TGG AAG TGG	96
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp	
20 25 30	
ATC CAC GAG CCC AAG GGC TAC CAT GCC AAC TTC TGC CTC GGC CCC TGC	144
Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys	
35 40 45	
CCC TAC ATT TGG AGC CTG GAC ACG CAG TAC AGC AAG GTC CTG GCC CTG	192
Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu	
50 55 60	
TAC AAC CAG CAT AAC CCG GGC GCC TCG GCG GCG CCG TGC TGC GTG CCG	240
Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro	
65 70 75 80	
CAG GCG CTG GAG CCG CTG CCC ATC GTG TAC TAC GTG GGC CGC AAG CCC	288
Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro	
85 90 95	
AAG GTG GAG CAG CTG TCC AAC ATG ATC GTG CGC TCC TGC AAG TGC AGC	336
Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser	
100 105 110	
TGA	339

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys	
1 5 10 15	
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp	
20 25 30	

Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys
35 40 45

Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu
50 55 60

Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro
65 70 75 80

Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro
85 90 95

Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: E. coli LC137/pPLMu.hTGF-beta2 (DSM5657)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..336
- (D) OTHER INFORMATION:/product= "human TGF-beta2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCT TTG GAT GCG GCC TAT TGC TTT AGA AAT GTG CAG GAT AAT TGC TGC	48
Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys	
115 120 125	
CTA CGT CCA CTT TAC ATT GAT TTC AAG AGG GAT CTA GGG TGG AAA TGG	96
Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp	
130 135 140	
ATA CAC GAA CCC AAA GGG TAC AAT GCC AAC TTC TGT GCT GGA GCA TGC	144
Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys	
145 150 155 160	
CCG TAT TTA TGG AGT TCA GAC ACT CAG CAC AGC AGG GTC CTG AGC TTA	192
Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu	
165 170 175	
TAT AAT ACC ATA AAT CCA GAA GCA TCT GCT TCT CCT TGC TGC GTG TCC	240
Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser	
180 185 190	

CAA GAT TTA GAA CCT CTA ACC ATT CTC TAC TAC ATT GGC AAA ACA CCC	288
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro	
195 . 200 205	
AAG ATT GAA CAG CTT TCT AAT ATG ATT GTA AAG TCT TGC AAA TGC AGC	336
Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser	
210 215 220	
TAA	339

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys	
1 5 10 15	
Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp	
20 25 30	
Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys	
35 40 45	
Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu	
50 55 60	
Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser	
65 70 75 80	
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro	
85 90 95	
Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser	
100 105 110	

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: E. coli LC137/pPLMu.htGF-beta3 (DSM 5658)

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION:1..336

(D) OTHER INFORMATION:/product= "human TGF-beta3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCT TTG GAC ACC AAT TAC TGC TTC CGC AAC TTG GAG GAG AAC TGC TGT	48
Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys	
115 120 125	
GTG CGC CCC CTC TAC ATT GAC TTC CGA CAG GAT CTG GGC TGG AAG TGG	96
Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp	
130 135 140	
GTC CAT GAA CCT AAG GGC TAC TAT GCC AAC TTC TGC TCA GGC CCT TGC	144
Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys	
145 150 155 160	
CCA TAC CTC CGC AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG	192
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu	
165 170 175	
TAC AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC GTG CCC	240
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro	
180 185 190	
CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT GTT GGG AGG ACC CCC	288
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro	
195 200 205	
AAA GTG GAG CAG CTC TCC AAC ATG GTG GTG AAG TCT TGT AAA TGT AGC	336
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser	
210 215 220	
TGA	339

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys	
1 5 10 15	
Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp	
20 25 30	
Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys	
35 40 45	
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu	
50 55 60	

Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro
 65 70 75 80
 Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro
 85 90 95
 Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "recombinant hybrid DNA of TGF-beta1 and TGF-beta3 DNA"

(vii) IMMEDIATE SOURCE:

- (B) CLONE: E. coli LC137/pPLMu.TGF-beta1(44/45)beta3

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..132
- (D) OTHER INFORMATION:/product= "N-terminal 44 amino acids of human TGF-beta1"

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:133..336
- (D) OTHER INFORMATION:/product= "C-terminal 68 amino acids of human TGF-beta3"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..336
- (D) OTHER INFORMATION:/product= "hybrid TGF-beta named TGF-beta1-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCC CTG GAC ACC AAC TAT TGC TTC AGC TCC ACG GAG AAG AAC TGC TGC	48
Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys	
1 5 10 15	
GTG CGG CAG CTG TAC ATT GAC TTC CGC AAG GAC CTC GGC TGG AAG TGG	96
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp	
20 25 30	
ATC CAC GAG CCC AAG GGC TAC CAT GCC AAC TTC TGC TCA GGC CCT TGC	144
Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Ser Gly Pro Cys	
35 40 45	

CCA TAC CTC CGC AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG	192
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu	
50 55 60	
TAC AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC GTG CCC	240
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro	
65 70 75 80	
CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT GTT GGG AGG ACC CCC	288
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro	
85 90 95	
AAA GTG GAG CAG CTC TCC AAC ATG GTG GTG AAG TCT TGT AAA TGT AGC	336
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser	
100 105 110	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys	
1 5 10 15	
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp	
20 25 30	
Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Ser Gly Pro Cys	
35 40 45	
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu	
50 55 60	
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro	
65 70 75 80	
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro	
85 90 95	
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser	
100 105 110	

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "recombinant hybrid DNA"

coding for hybrid TGF-beta2-3"

(vii) IMMEDIATE SOURCE:

(B) CLONE: E. coli LC137/pPLMu.TGF-beta2(44/45)beta3.

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION:1..132

(D) OTHER INFORMATION:/product= "N-terminal 44 amino acids of human TGF-beta2"

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION:133..336

(D) OTHER INFORMATION:/product= "C-terminal 68 amino acids of human TGF-beta3"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..336

(D) OTHER INFORMATION:/product= "hybrid TGF-beta2-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCT TTG GAT GCG GCC TAT TGC TTT AGA AAT GTG CAG GAT AAT TGC TGC	48
Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys	
1 5 10 15	
CTA CGT CCA CTT TAC ATT GAT TTC AAG AGG GAT CTA GGG TGG AAA TGG	96
Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp	
20 25 30	
ATA CAC GAA CCC AAA GGG TAC AAT GCC AAC TTC TGC TCA GGC CCT TGC	144
Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ser Gly Pro Cys	
35 40 45	
CCA TAC CTC CGC AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG	192
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu	
50 55 60	
TAC AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC GTG CCC	240
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro	
65 70 75 80	
CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT GTT GGG AGG ACC CCC	288
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro	
85 90 95	
AAA GTG GAG CAG CTC TCC AAC ATG GTG GTG AAG TCT TGT AAA TGT AGC	336
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser	
100 105 110	

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys
1 5 10 15
Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp
20 25 30
Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ser Gly Pro Cys
35 40 45
Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu
50 55 60
Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro
65 70 75 80
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro
85 90 95
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "recombinant hybrid DNA
coding for hybrid TGF-beta3-2"

(vii) IMMEDIATE SOURCE:
(B) CLONE: E. coli LC137/pPLMu.TGF-beta3(44/45)beta2

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..132
(D) OTHER INFORMATION:/product= "N-terminal 44 amino
acids of human TGF-beta3"

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:133..336
(D) OTHER INFORMATION:/product= "C-terminal 68 amino
acids of human TGF-beta2"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..336

(D) OTHER INFORMATION:/product= "hybrid TGF-beta3-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCT TTG GAC ACC AAT TAC TGC TTC CGC AAC TTG GAG GAG AAC TGC TGT	48
Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys	
1 5 10 15	
GTG CGC CCC CTC TAC ATT GAC TTC CGA CAG GAT CTG GGC TGG AAG TGG	96
Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp	
20 25 30	
GTC CAT GAA CCT AAG GGC TAC TAT GCC AAC TTC TGT GCT GGA GCA TGC	144
Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ala Gly Ala Cys	
35 40 45	
CCG TAT TTA TGG AGT TCA GAC ACT CAG CAC AGC AGG GTC CTG AGC TTA	192
Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu	
50 55 60	
TAT AAT ACC ATA AAT CCA GAA GCA TCT GCT TCT CCT TGC TGC GTG TCC	240
Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser	
65 70 75 80	
CAA GAT TTA GAA CCT CTA ACC ATT CTC TAC TAC ATT GGC AAA ACA CCC	288
Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro	
85 90 95	
AAG ATT GAA CAG CTT TCT AAT ATG ATT GTA AAG TCT TGC AAA TGC AGC	336
Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser	
100 105 110	

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys	
1 5 10 15	
Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp	
20 25 30	
Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ala Gly Ala Cys	
35 40 45	
Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu	
50 55 60	
Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser	
65 70 75 80	

Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Ile	Gly	Lys	Thr	Pro
				85	"				90					95	
Lys	Ile	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Lys	Ser	Cys	Lys	Cys	Ser
			100					105					110		

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCGGAATTCC GG

12